

1/24

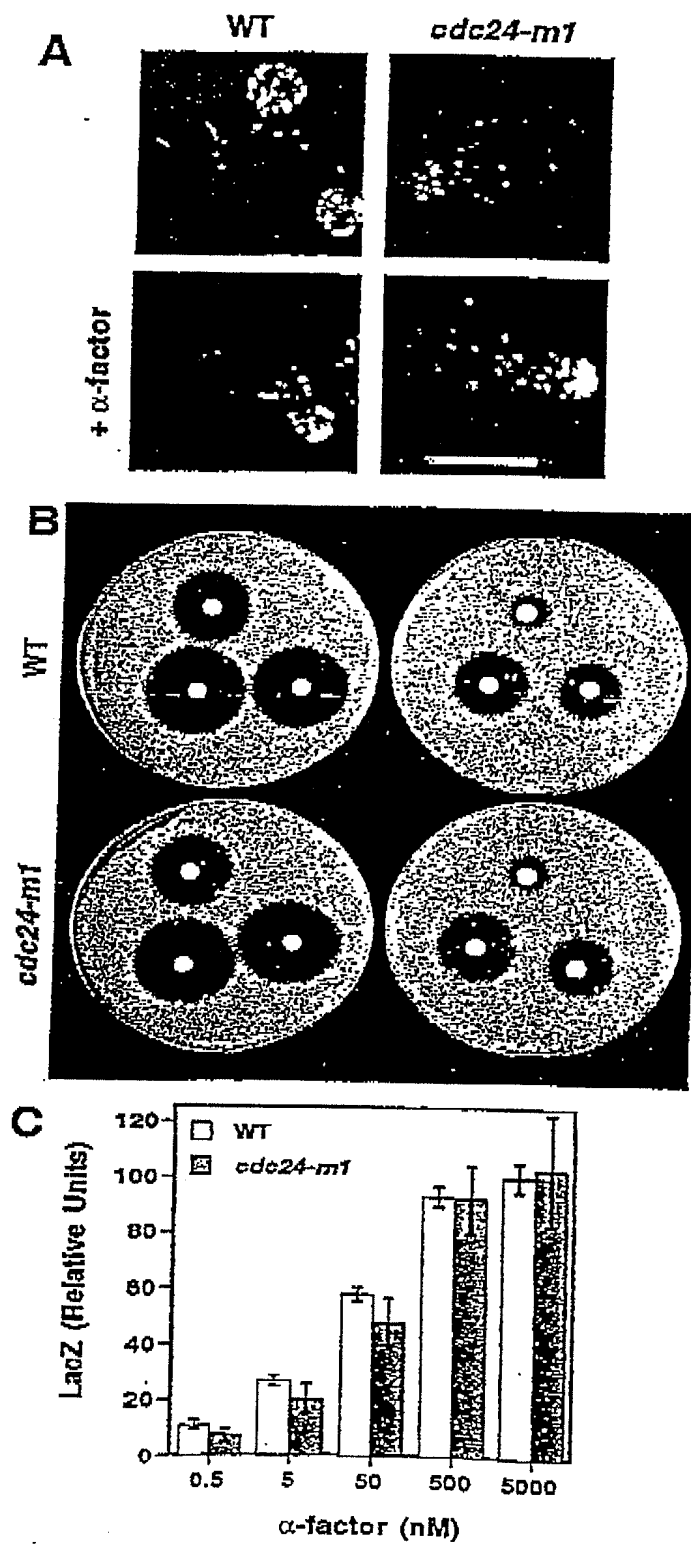


FIG. 1

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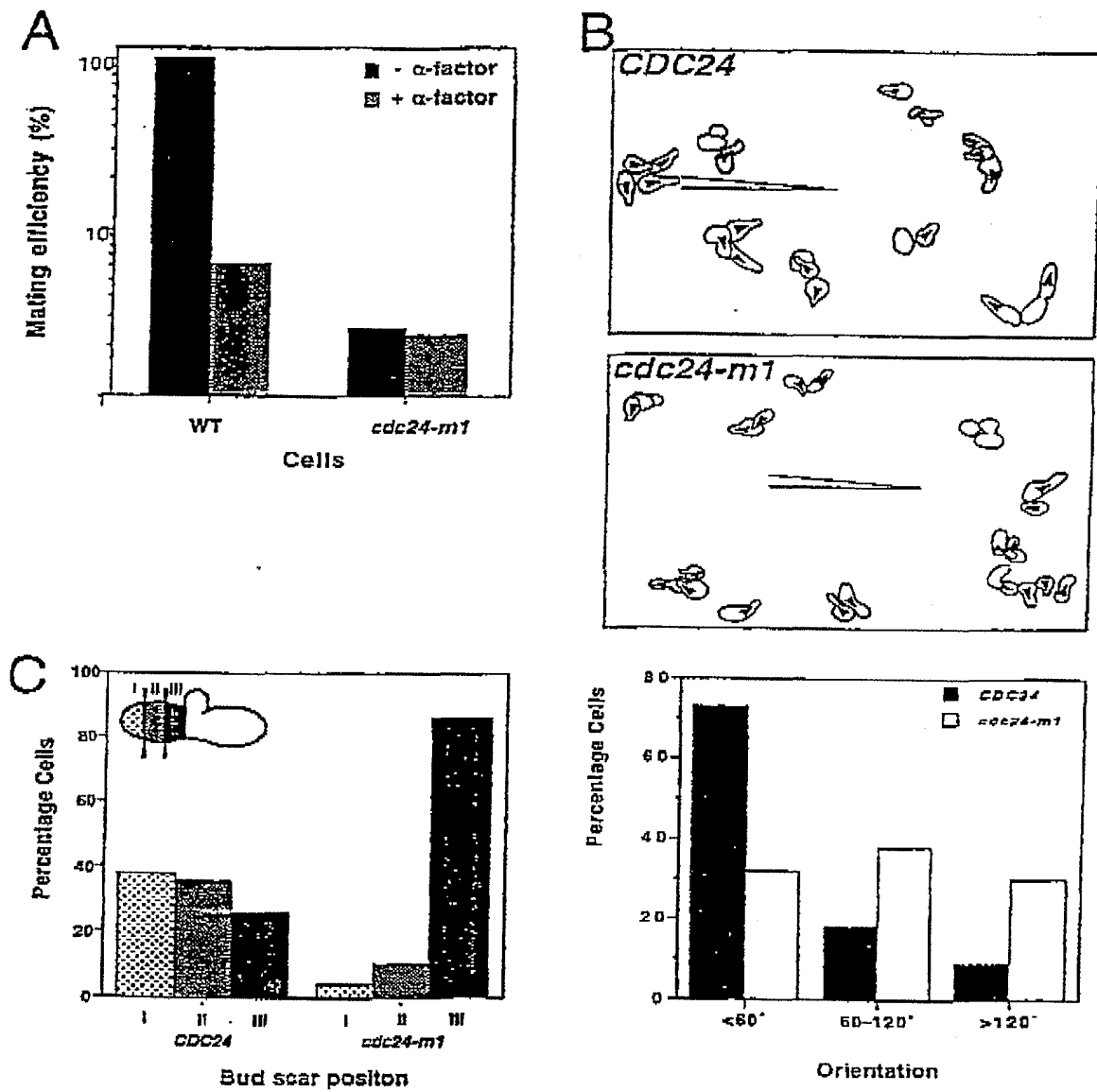


FIG. 2

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**A**

Cdc24-m1 QFKLPVIAVDLKVCKKSI  
 Cdc24-m2 QFKLPVIAAGDLKVCKKSI  
 Cdc24-m3 QFKLPVIAVDLKVCKKSI  
 Cdc24 Sc 181 QFKLPVIAVDLKVCKKSI 189  
 |... ||-| .||| |-|  
 DB Hu 385 QYEFDVILSPFLKVQKTY 403

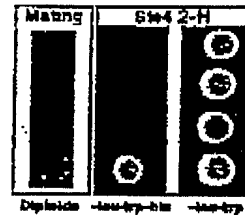
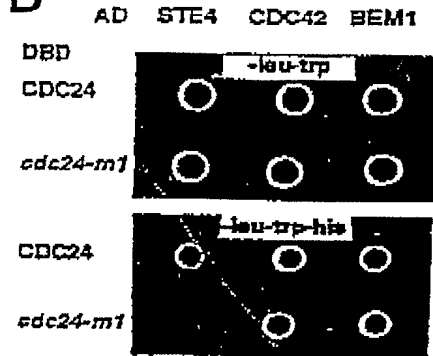
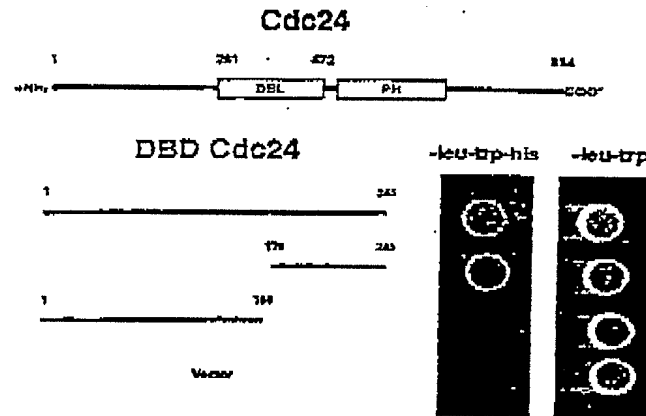
**B****C****D**

FIG. 3

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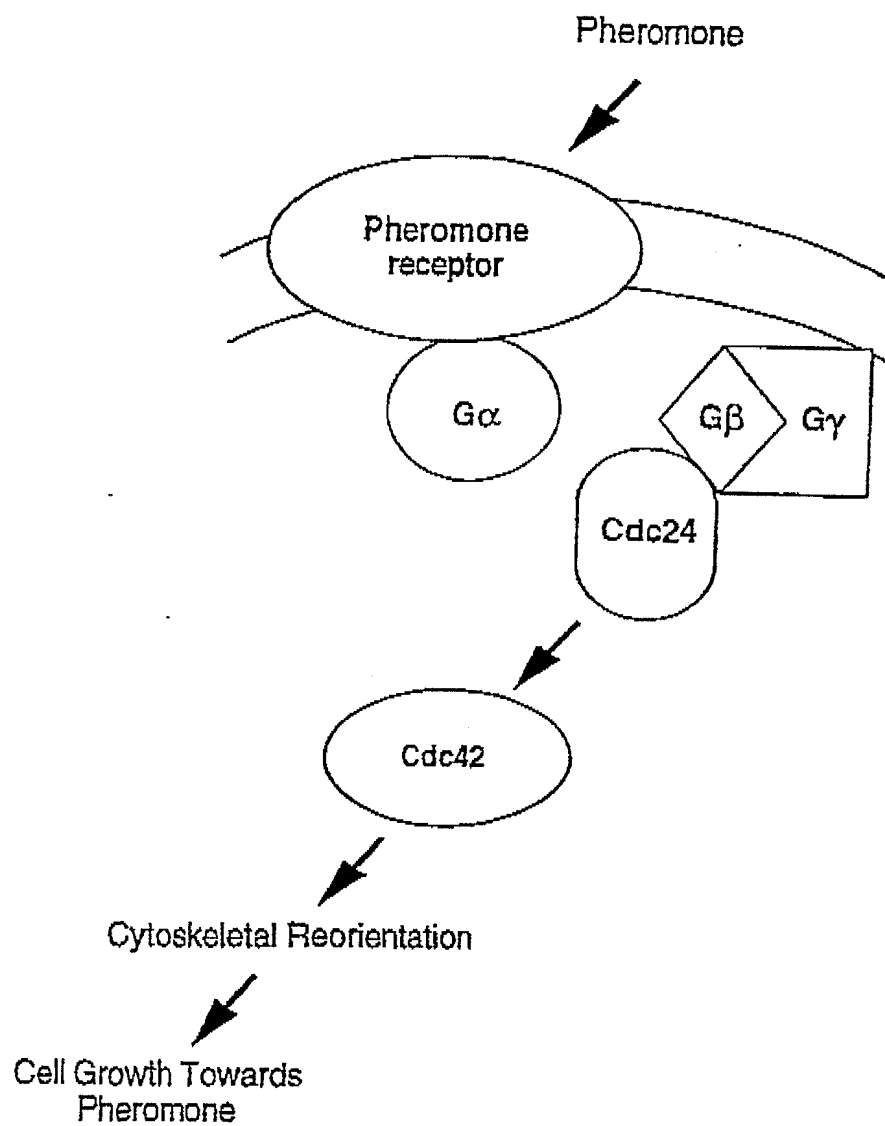


FIG. 4

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Figure 5

5	2113/1	ATG GAA CAT CCA CCA GCA GCT CTC AGA ACA	2143/11	TTT TCA ACC CAA TCA ACT TCA TCT TTG AAT
	M E H P P A A L R T		F S T Q S T S S L N	
10	2173/21	TCA GTA AGT ACT GTT TCG TCT TCA AGA ATT	2203/31	GTT TCT CTG GGC CCA GTC AAT ATA AAC AAT
	S V S T V S S S R I		V S S G P V N I N N	
	2233/41	TTC AAT AAA CCA AGT ACT CCC AAA GAC CAT	2263/51	TTA TTC TAT CGA TGT GAA TCA CTA AAA CGA
	F N K P S T P K D H		L F Y R C E S L K R	
15	2293/61	AAA CTA CAA AAA ATC CCT GGC ATG GAA CCA	2323/71	TTT TTG AAC CAA GCT TTC AAT CAG GCT GAA
	K L Q K I P G M E P		F L N Q A F N Q A E	
	2353/81	CAA CTC AGT GAA CAA CAA GCA TTG GCT TTG	2383/91	GCA CAG GAA AGA AGC AAT GGA AAT GGA CAT
20	Q L S E Q Q A L A L		A Q E R S N G N G H	
	2413/101	AGT AAT GGC AAA CGT CAT CAA TCA TTA GAC	2443/111	GGT GCC ATG AAT AGA CTT TCA GTT GGT TCT
	S N G K R H Q S L D		G A M N R L S V G S	
25	2473/121	GAT AGT AGT TCG ATC CAA GGT TCA TTG ACA	2503/131	CGA ATG GCC ACC AAT GCG TCA ACG TCA TCT
	D S S S I Q G S L T		R M A T N A S T S S	
	2533/141	TTA ATC AGT GGT ATG CCA AAC AAC AAC ACT	2563/151	TTA TTT ACG TTT ACT GCA GGG GTT TTA CCA
30	L I S G M P N N N T		L F T F T A G V L P	
	2593/161	GCT AAT ATT AGT GTC GAT CCT GCT ACC CAT	2623/171	CTT TGG AAA TTG TTC CAA CAA GGG GCC CCC
	A N I S V D P A T H		L W K L F Q Q G A P	
	2653/181	TTT TGT GTT CTT ATC AAT CAT ATC CTT CCT	2683/191	GAT TCC CAA ATA CCA GTT GTC AGT TCT GAT
35	F C V L I N H I L P		D S Q I P V V S S D	
	2713/201	GAC TTG AGA ATT TGC AAA AAA TCA GTA TAT	2743/211	GAC TTT TTA ATT GCC GTC AAG ACA CAA TTG
	D L R I C K K S V Y		D F L I A V K T Q L	
40	2773/221	AAT TTT GAT GAC GAG AAT ATG TTC ACT ATA	2803/231	TCC AAT GTT TTC TCC GAC AAT GCC CAA GAT
	N F D D E N M F T I		S N V F S D N A Q D	
	2833/241	TTA ATC AAG ATT ATT GAT GTC ATT AAT AAA	2863/251	CTA CTT GCT GAG TAC TCA GAT GCT AGT GAC
45	L I K I I D V I N K		L L A E Y S D A S D	
	2893/261	CTG GGT GGT GGC GAT GAA GAT GTA AAT ATG	2923/271	GAT GTT CAA ATT ACC GAT GAA AGA TCA AAA
	S G G G D E D V N M		D V Q I T D E R S K	
	2953/281	GTT TTC CGA GAA ATT ATC GAA ACA GAA AGA	2983/291	AAA TAT GTT CAA GAC TTG GAA CTA ATG TGT
50	V F R E I I E T E R		K Y V Q D L E L M C	
	3013/301	AAA TAC CGT CAA GAT CTA ATT GAA GCC GAA	3043/311	AAT TTG TCT TCA GAA CAA ATT CAC TTG TTA
	K Y R Q D L I E A E		N L S S E Q I H L L	
55	3073/321	TTC CCA AAT TTA AAT GAG ATT ATT GAT TTT	3103/331	CAA AGA CGA TTC CTC AAT GGG TTA GAA TGT
	F P N L N E I I D F		Q R R F L N G L E C	
	3133/341	AAC ATC AAT GTA CCT ATT AGA TAT CAA AGA	3163/351	ATT GGA TCA GTA TTT ATT CAT GCT TCT TTG
60	N I N V P I R Y Q R		I G S V F I H A S L	
	3193/361	GGC CCT TTC AAT GCT TAT GAA CCT TGG ACT	3223/371	ATA GGA CAA TTG ACG GCG ATT GAT TTG ATC
	G P P N A Y E P W T		I G Q L T A I D L I	
	3253/381	AAC AAA GAA GCT GCT AAT TTG AAA AAA TCG	3283/391	TCA AGT CTA CTT GAT CCT GGG TTT GAA CTT
65	N K E A A N L K K S		S S L L D P G F E L	
	3313/401	CAA TCG TAT ATA TTA AAG CCG ATC CAA AGA	3343/411	TTG TGT AAA TAC CCA CTT TTG TTG AAA GAG
	Q S Y I L K P I Q R		L C K Y P L L L K E	
	3373/421	TTA ATC AAA ACA TCA CCA GAA TAT TCA AAA	3403/431	CAG GAC CCC CAT GGC AGC TCG TCA TCG ACA
70	L I K T S P E Y S K		Q D P H G S S S S T	
	3433/441	TCA TTC AAT GAA TTA TTG GTG GCT AAA ACT	3463/451	GCA ATG AAA GAA TTG GCA AAT CAA GTC AAT
	S F N E L L V A K T		A M K E L A N Q V N	

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	3493/461	GAG GCG CAA AGA CGA GCA GAA AAT ATC GAA	3523/471	CAT TTG GAA AAA CTA AAA GAA AGA GTA GGT
	E A Q R R A E N I E	H L E K L K E R V G		
5	3553/481	AAT TGG CGT GGG TTT AAT TTG GAT GCT CAA	3583/491	GGA GAA CTA TTA TTC CAC GGA CAA GTT GGG
	N W R G F N L D A Q	G E L L F H G Q V G		
	3613/501	GTT AAA GAT GCT GAA AAT GAA AAG GAA TAC	3643/511	GTT GCT TAT CTT TTT GAA AAA ATC GTA TTT
10	V K D A E N E K E Y	V A Y L F E K I V F		
	3673/521	TTT TTC ACA GAA ATT GAT GAT ACC AAA AAA	3703/531	TCT GAT AAA CAG GAA AAG AAG AGC AAG TTT
	F F T E I D D T K K	S D K Q E K K S K F		
	3733/541	TCG ACA AGA AAG AGA TCA ACT TCA TCA AAT	3763/551	CTT AGT TCA TCG ACT ACT AAT TTG TTG GAA
15	S T R K R S T S S N	L S S S T T N L L E		
	3793/561	TCA ATA AAC AAT TCC CGA AAG GAT AAC ACA	3823/571	TTG CCA TTG GAA TTA AAG GGA AGA GTT TAT
	S I N N S R K D N T	L P L E L K G R V Y		
20	3853/581	ATA TCG GAG ATT TAT AAC ATT TCC GCA CCA	3883/591	AAC ACT CCT GGC TCA ACT CTA ATC ATC TCA
	I S E I Y N I S A P	N T P G S T L I I S		
	3913/601	TGG TCA GGT AGA AAG GAA AGC GGC TCA TTC	3943/611	ACT TTG AGA TAT CGT AGT GAA GAA GCC AGA
25	W S G R K E S G S F	T L R Y R S E E A R		
	3973/621	AAC CAA TGG GAA AAG TGT TTA CGT GAT TTG	4003/631	AAG ACT AAT GAA ATG AAT AAA CAA ATT CAT
	N Q W E K C L R D L	K T N E M N K Q I H		
	4033/641	AAG AAG TTA CGT GAT TCC GAC CTG TCA TTT	4063/651	AAT ACT GAT GAC TCT GCC ATA TAT GAT TAC
30	K K L R D S D S S F	N T D D S A I Y D Y		
	4093/661	ACG GGT ATT AGT ACG TCA CCA GTC AAT CAA	4123/671	TCA ACT CAA CAA CAA TAC TAT GAT CAT CGG
	T G I S T S P V N Q	S T Q Q Q Y Y D H R		
	4153/681	GGC TCT CAC AGT TCC CCG CAT CAC TCA TCG	4183/691	TCA TCC ACT TTG AGT ATG ATG AAG AAT AAT
35	G S H S S R H H S S	S S T L S M M K N N		
	4213/701	AGA GTT AAA TCT GGT GAT TTG AGT AGA ATA	4243/711	TCT TCA ACT TCA ACA ACA TTA GAT TCT TTC
	R V K S G D L S R I	S S T S T T L D S F		
40	4273/721	AGT AAC AAC TTG AAT GGG TCA CCA AAT ACC	4303/731	ACT AAT CCA TCT TTG ATG TCT TCA GAT GCC
	S N N L N G S P N T	T N P S L M S S D A		
	4333/741	ACC AAA ACA ATT CCA ACA TTT GAC GTT GCA	4363/751	ATT AAA TTG CTT TAC AAA TCG ACA GAA TTG
45	T K T I P T F D V A	I K L L Y K S T E L		
	4393/761	TCA GAG CCA TTG ATT GTC AAT GCA CAA ATT	4423/771	GAG TAT AAT GAC CTT TTA CAG AAA ATT ATC
	S E P L I V N A Q I	E Y N D L L Q K I I		
	4453/781	TCC CAG ATT ATC ACT TCG AAC TTG GTG GCA	4483/791	GAT GAT GTC AAT ATT AGT CGA TTG AGA TAT
50	S Q I I T S N L V A	D D V N I S R L R Y		
	4513/801	AAA GAC GAC GAA GGA GAC TTT GTG AAT TTG	4543/811	AAT TCA GAT GAT GAT TGG GGG TTA GTG CTT
55	K D D E G D F V N L	N S D D D W G L V L		
	4573/821	GAT ATG TTA ACC AGT GAA GAC TTT TAC CAA	4603/831	ACA TCA AGC AAT GAA AAA CGA CTG GTG ACA
	D M L T S E D F Y Q	T S S N E K R S V T		
	4633/841	GTG TGG GTT TCT TGA		
60	V W V S *			

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Figure 6

5 Blastp line up of S.c. Cdc24p and C.a. Cdc24p

S.c. Cdc24p: 1 MAIQ---TR-FA 8  
M R P+

10 C.a. Cdc24p: 1 MEHPAALRTFSTQ 14

S.c. Cdc24p: 9 SGTSLSDLKPKPSATSIIPMQNV--MNKPVTEQDSLPHICANIRKRLEVLPOLKPFLLQ 66  
S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL

C.a. Cdc24p: 15 STSSLNSVSTVSSSRIVSSGPVNINNFNKPSTPKDHLFYRCESLKRKLQKIPGMEPFLLQ 74

15 S.c. Cdc24p: 67 AYQSSEVLSEKQSLLSQKQHQELLKSNGANRSDSLAP--TLRSSSISTATSLMSMEG 123  
A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M

C.a. Cdc24p: 75 APNQAEQLSEQQALALAQERSNGNGHSNGKRHQSLDGAMNRLSVGSDSSSIQGSLTRMAT 134

S.c. Cdc24p: 124 ISYTSNPSATPNMEDTLTTFMSGILPITMDCDFVTQLSOLFQOGAPLCILFNSVKPQFK 183  
+ T+S S PN +TL TF+ G+LP + DP T L +LFQOGAP C+L N + P +

20 C.a. Cdc24p: 135 NASTSSLISGMPN--NNTLFTFTAGVLPANISVDPATHLWKLFOQGAFCVLINHLPSQ 193

S.c. Cdc24p: 184 LPVIASDDLKVCKKSIYDFILGCKKHPAFNDEELFTISDVFNSTSQLVKVLEVVELTMN 243  
+PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+

25 C.a. Cdc24p: 194 IPVVSSDDLRIKKSVDYDFLIAVKTQLNFEDDENMFTISNVFSDNAQDLIKIIDVINKLLA 253

S.c. Cdc24p: 244 SSPTIFPSKSKTQIMNAENQHRHQPQSSKKHNEYVKIIEFVATERKYVHDLEILDKY 303  
S + + + +E K+ +E + TERKYV DLE++ KY

30 C.a. Cdc24p: 254 EYSDASDSGGGDEEDV-----NMDVQITDERSKVFREIETERKYVQDLELMCKY 302

S.c. Cdc24p: 304 RQQLLDSNLITSEELYMLFPNLGDAIDFORRFLISLEINALVEPSKQIRIGALFMH-SKHF 362  
RQ L+++ ++SE++++LFPNL + IDFORRFL LE N V ORIG++F+H S

C.a. Cdc24p: 303 RQDLIEAENLSSEQIHLFPNLNEIIDFORRFLNGLECNINVPYRQIRIGSVFIHASLGP 362

35 S.c. Cdc24p: 363 FKLYPEWSIGONAAIEFLSSTLHKMRVDESQRFIINNKLELQSFYKPVORLCRYPLLK 422  
F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K

C.a. Cdc24p: 363 FNAYEPWTIGQLTAIDLINKEAANDKKSSS--LLDPGFELQSYILKPIQRLCKYFLLK 419

40 S.c. Cdc24p: 423 ELLAE-----SSDDNNTKELEAALDISKNIARSINENQRRTENHQVVKLYGRV 471  
EL+ SS + EL A K +A +NE QRR EN + ++KL RV

C.a. Cdc24p: 420 ELIKTSPEYSKQDPHGSSSSTSFNELLVAKTAMKELANQVNEAORRAENIEHLEKLKERV 479

S.c. Cdc24p: 472 VNWKGYRISKFGELLYFDKVFISTNSSSEPEREFVYLFEKIILFSEVVTKKSASSLI 531  
NW+G+ + GELL+ +V + +E E+E+ YLFEDI+ F+E+ K +

45 C.a. Cdc24p: 480 GNWRGFNLDAQELLFHGQGV---KDAENEKEYVAYLFEDIKIVFFTEIDDTKKSDKQE 535

S.c. Cdc24p: 532 LKKKSSTASISASNITDNGSPHSHYKRRHSNSSSSNNIHLSSSSAAAIHSSSTNSSDN 591  
K K ST ++SN+ SSS ++ S NS +

50 C.a. Cdc24p: 536 KSKFSTRKRSTSSNL-----SSSTTNLLESINNSRKD 568

S.c. Cdc24p: 592 NSNNSSSSSLFKLSANEPKLDLGRIMIMNLNQIIPQN--NRSLNITWESIKEQGNFLK 649  
N+ L+L+GR+ I + I N +L I+W KE G+F L+

C.a. Cdc24p: 569 NT-----LPLELKGVRVYISEIYNISAPNTPGSTLIISWGRKESGSFTLR 613

55 S.c. Cdc24p: 650 FKNEETRDNWSSCLQQLIHDLKNEQFKARHHSSTSTSS-----TAKSSSMMSPTTT 701  
+++EE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T

C.a. Cdc24p: 614 YRSEEARNQWEKCLADLKTNEMNKQIHKKLKRDSDSSFNDDSAIYDYGISTSPVNQSTQ 673

60 S.c. Cdc24p: 702 MNTPNHNSRQT--HDSMASFSSSHMKRVS----DVLPRKRTTSSSFESEIKS----- 748  
+H S + H S ++ S RV + TT SF + +

C.a. Cdc24p: 674 QQYYDHRGSHSSSRHSSSTLSMMKNRVKSGDLSRISSTSTTLDSFNNLNGSPNTTNP 733

S.c. Cdc24p: 749 --ISENFKNSIPESILFRISYNNNSNTSSSEIFTLLVEKVVNFPDDLIMAINSKI--SN 804  
+S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN

65 C.a. Cdc24p: 734 SLMSSDATKTIPTFDVAIKLLY----KSTELSE--PLIVNAQIEYNDLLQKIISQIITSN 787

S.c. Cdc24p: 805 THNNNISPIKIKYQDEGDGDFVVLGSDDEDWNVAKEMLAENNEKFLNIRLY 854  
++++ I++++Y+D++GDFV L SD+DW + +ML + F +

C.a. Cdc24p: 788 LVADDVN--ISRLRYKXDEGDFVNLNSDDDWGLVLDMLTSED--FYQTSSNEKRSVTVWVS 844

Figure 7a

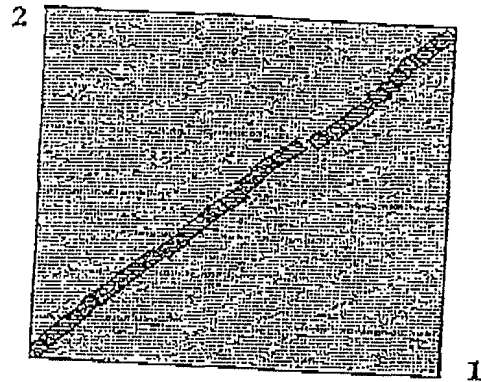
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## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix: 0.BLOSUM62 gap open: 11 gap extension: 1  
 x\_dropoff: 50 expect: 10.0 wordsize: 3 Filter: ☐ Align:

Sequence 1 lc|S.c. Cdc24p Length 854 (1..854)

Sequence 2 lc|C.a. Cdc24p Length 844 (1..844)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 446 bits (1136), Expect = e-124

Identities = 288/881 (32%), Positives = 464/881 (51%), Gaps = 112/881 (12%)

```

Query: 9  SGTSLSDLKPKPSATSISIPMQNV--MNKPVTEQDSLPHICANIRKRLEVLPLQKPFLOL 66
      S +SL+ + S+ +S N+ NKP T +D LF+ C +++++L+ +P ++PFL
Sbjct: 15 STSSLNSVSTVSSSRIVSSGPNINNNFNKPSPTPKDHLFYRCESLKRKLQKIPGMEFFLNQ 74

Query: 67 AYQSSEVLSEKSLLLSQKHQELLSKNGANRDSDDLAP---TLRSSSISTATSLMSMEG 123
      A+ +E LSE+Q+L L+Q++ SNG S D A ++ S S S SL M
Sbjct: 75 AFNQAEQLSEQQALALAQERSNGNGHSNGKRHQSLDGAMNRLSVGSDSSSIQGLTRMAT 134

Query: 124 ISYTSNPSATPNMEDTLTFSMGLPITMDCDPVTQLSOLFQQGAPLCILFNSVKPQFK 183
      + T+S S PN +TL TF+ G+LP + DP T L +LFQQGAP C+L N + P +
Sbjct: 135 NASTSSLISGMPN--NNTLFTFTAGVLPANISVDPATHLWKLFQQGAPFCVLINHLPSQ 193

Query: 184 LPVIASDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFNSTSQLVKVLEVVELTMN 243
      +PV++SDDL++CKKS+YDF++ K F+DE +FTIS+VF+++ L+K+++V+ L+
Sbjct: 194 IPVVSSDDLRIKKSVDYFLIAVKTQLNFDENMFTISNVFSDNAQDLIKIIDVINKLLA 253

Query: 244 SSPTIFPSKSKTQQIMNAENQHRHQPOQSSKKHNEYVKIIKEFVATERKYVHOLEILDY 303
      S + + + +E K+ +E + TERKYV DLE++ KY
Sbjct: 254 EYSDASDSGGGDEDV-----NMDVQITDERSKVFRETIETERKYVQDLELMCKY 302

Query: 304 RQQLDSNLITSEELYMLFPNLGDAIDFQRRFLISLEINALVEPSKORIGALFMH-SKHF 362
      RQ L+++ ++SE++++LFPNL + IDFQRRFL LE N V ORIG++F+H S
Sbjct: 303 RQDLIEAENLSSEQIHLLFPNLNEIIDFQRRFLNGLECNINVPRIYQRIQSVFIHASLGP 362

Query: 363 FKLYEPWSIGQNAIEFLSSTLEKMRVDESQRFTIINNKLQSFYKPVQRLCRYPLLVK 422
      F YEPW+IGQ AI+ ++ ++ S +++ ELQS++ KP+QRLC+YPLL+K
Sbjct: 363 FNAYEPWTIGQLTAIDLINKEAANLKKSSS---LLDPGEFLQSVYK
  
```



f Figure 7a cont.

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Query: 423 ELLAE-----SSDDNNTKELEAALDISKNIARSINENQRRTENHQVVKKLYGRV 471  
 EL+ SS + EL A K +A +NE QRR EN + ++KL RV  
 Sbjct: 420 ELIKTSPEYSKQDPHGSSSSSTSFNELLVAKTAMKELANQVNEAQRRAENIEHLEKLERV 479

Query: 472 VNWKGYRISKFGELLYFDKVFISTYNSSEPEREFVYLFEEKIILFSEVVTKKSASSLI 531  
 NW+G+ + GELL+ +V + +E E+E+ YLFEEKI+ F+E+ K +  
 Sbjct: 480 GNWRGFNLDAQGELLFHGQVGV----KDAENEKEYVAYLFEEKIVFFPTEIDDTKKSQKQE 535

Query: 532 LKXKSSTASISASNITDNNGSPHSHYHKRHSNSSSSNNIHLSSSSAAAIHSSSTNSSDN 591  
 K K ST ++SN+ SSS ++ S NS +  
 Sbjct: 536 KSKFTSTRKRSTSSNL-----SSSTTNLLESINNSRKO 568

Query: 592 NSNNSSSSSLFKLSANEPKLDLRGRIMIMNLNQIIPQN--NRSLNITWESIKEQGNFLK 649  
 N+ L+L+GR+ I + I N +L I+W KE G+F L+  
 Sbjct: 569 NT-----LPLELKGRVYISEIYNISAPNTFGSTLIISWSCRKESGSPTLR 613

Query: 650 FKNEETRDNWSSCLQQLIHDLKNEQFKARHHSSTSTSS-----TAKSSSMSPPTT 701  
 +++EE R+ W CL+ L + N+Q + S S+ ++ T S+S ++ +T  
 Sbjct: 614 YRSEARNQWEKCLRDLDKTNEMNKQIHKKLRDSDSSPNTDDSAIYDYTGISTSPVNQSTQ 673

Query: 702 MNTPNHHNSRQT--HDSMASPSSSHMKRVS----DVLPRRTTSSSPSESIKS----- 748  
 +H S + H S ++ S RV + TT SF + +  
 Sbjct: 674 QQYVDHRCSEHSSRHSSSSTLSMMKNRVKSGDLSRISSTSTTLDSFNNLNGSPNTTNP 733

Query: 749 --ISENFKNIPESILFRISYNNNSNNTSSSEIPTLLVEKVWNFDDLYMAINSKI--SN 804  
 +S + +IP + ++ Y +T SE L+V ++DL+ I S+I SN  
 Sbjct: 734 SLMSSDATKTIPTFDVAIKLLY----KSTELSE--PLIVNAQIEYNLLQKIISQIITSN 787

Query: 805 THNNNISPIKIKYODEDGDGVVLGSDDEDWNVAKEMLAENN 845  
 ++++ I++++Y+D++GDFV L SD+DW + +ML +  
 Sbjct: 788 LVADDVN-ISRLRYKDDGDFVNLNSDDDWGLVLDMLTSED 827

CPU time: 0.26 user secs. 0.02 sys. secs 0.28 total secs.

Gapped  
 Lambda K H  
 0.270 0.0470 0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 12253

Number of Sequences: 0

Number of extensions: 709

Number of successful extensions: 15

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 844

length of database: 90,077,593

effective HSP length: 63

effective length of query: 781

effective length of database: 83353792

effective search space: 65099311552

effective search space used: 65099311552

T: 9

A: 40

X1: 16 ( 7.2 bits)

X2: 128 (49.9 bits)

X3: 128 (49.9 bits)

S1: 42 (21.9 bits)

S2: 73 (32.8 bits)

Figure 7b

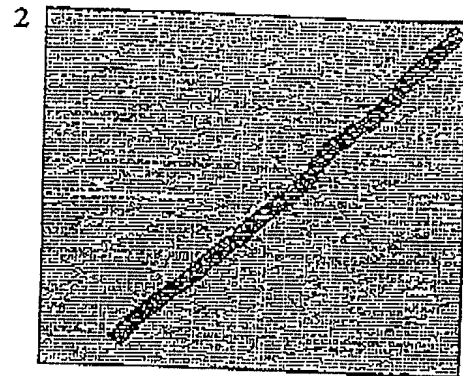
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## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.0.9 [May-07-1999]

Matrix: 0-BLOSUM62 gap open: 11 gap extension: 1  
 x\_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☐ Align

Sequence 1 lcl|S.c. Cdc24p Length 854 (1..854)

Sequence 2 lcl|S.p. Cdc24p Length 834 (1..834)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 238 bits (601), Expect = 1e-61

Identities = 212/760 (27%), Positives = 348/760 (44%), Gaps = 94/760 (12%)

```

Query: 156 DFVTQLSQLFQQGAPLCILFNSVXKPOKPLFVIASDDLK---VCKKSIYDFILGCKKHFAF 212
          + G PLC LEN + + KL V +S L+ VCK S+Y F+L CK
Sbjct: 67 DPVTEIWLFCRLGYPLCALFNCLPVKQKLEVNSSVSLENTNVCKASLYRFMLMCKNELGL 126

Query: 213 NDEELFTISDVFANSTSQLVKVLEVETLMNSSPTIFFPSKSKTQQIMNAENQERHQPQQS 272
          D LF+IS+++ ST+ LV+ L+ +E L+ +KS + + ++ S
Sbjct: 127 TDAALFSISEIXKPSTAPLVRALQTIELLLKKYEVSNNTKSSSTPSPSTDDNVPTGTILNS 186

Query: 273 SKKHNEYVKLIKEFVATERKYVHDLEILDKYRQQLLDSNLITSEELYMLFPNLGDAIDFQ 332
          ++ E TE KY+ DLE L Y L +++ + + +F NL + +DFQ
Sbjct: 187 LIASGR--RVTAELYETELKYIQDLEYLSNYMVILQQKQILSQDTILSIFTNLNEILDFO 244

Query: 333 RRFLISLEINALVEPSKORIGALFMHSHKHFPLYEPWSIG-QNAATEFLSSTLHKMRVDE 391
          RRFL+ LE+N + +QR+GALF+ + F +Y+ + .NA + + ++V
Sbjct: 245 RFLVGLMNLSLPVEEQRLCALFIALEEGFSVYQVFCTNFPNAQQLIIDNQQLLKVAN 304

Query: 392 SQRFIINNKLQSFLYKPVQRLCRYPLLVKELL-AESSDDNNTKEPAALDISKNIAARS 450
          ++ EL + L KP+QR+C+YPLL+ +LL S +EL+ + +A
Sbjct: 305 ----LLEPSYELPALLIKPIQRICKYPLLLNQLLKGTPSGYQYEEELKQGMACVVRVANQ 360

Query: 451 INENQRRTENHQVVKKLYGRVNVNWKGYRISKFGELLYFDKVPISTNSSSEPEREFEVYL 510
          +NE +R EN + +L RV++WKGY + FG+LL +D V + ++ ERE+ VYL
Sbjct: 361 VNETRRIHENRNAIIIELEQRVIDWKGYSLOQYFGQLLVWDVVNV----CKADIEREYHVYL 416

Query: 511 FEKIIILFSEVVT-KKSASSLILKKKSSTSA$-----ISASNITDN----- 550
          FEKI++ E+ T K+ A S+ + KK+ S I SNIT
Sbjct: 417 FEKILLCKEMSTLKRQARSISMNKKTKRLDSLOIKGRITSNITTHIDV
  
```

Figure 7b cont..

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Query: 551 --NGSPHSHYHKRHSNSSSSNNIHL-----SSSAAAIHSSTNSSDNNNSNNSSSS 599  
 G P H + S+ + +S + I S+ ++ N N SSS  
 Sbjct: 477 FWRGDPQHESFILKLNEESHKLWMSVLNRLWLKNEHGSFKDIRSAASTPANPVYNRSSS 536

Query: 600 SLFKLSANEPKLD-LRGRIMIMNLN---QIIPQNNRSLNITWESIKEQGNFLLKPKNEET 655  
 K N D LR + N+N I +++S T + K+ K+ T  
 Sbjct: 537 QTSK-GYNSSDYDLLRTHSLDENVNSPTSISSPSSKSSPFTKTTSKDT-----KSATT 588

Query: 656 RDNWSSCLOQLIHDLKNEQFKARHHSSTST-----TSSTAKSSSMMSPTTTMNT--PNHH 708  
 D S +L + R +TST +SSTA S +S + +N+ +++  
 Sbjct: 589 TDERPSPDFIRLNSEESVGTSSLRTSQTSTIVSNDSSSTASIPSQISRISQVNSLLNDYN 648

Query: 709 NSRQTH-----DSMASF-----SSSHMKRVSD-----VLPKRRTTSSSPFESE 745  
 +RQ+H S++ F SSS +++ D + P++ + S+ +S+  
 Sbjct: 649 YNRQSHITRVYSGTDDGSSVSIFEDTSSSTKQKIFDQPTTNDCDVMRPRQYSYSAGMKSD 708

Query: 746 IKSISENFKNSIPESSILFRISYNNNSNNTSSSEI-----FTLLVEKVWNFDDLLIMAINSK 801  
 + S+ SS +S N +N + L+V FD+L+ + K  
 Sbjct: 709 GSLLPSTKHTSLSSSSTSTSLSVRNTTNVKIRLRLHEVSLVLVVARDDITFDLLAKVEHK 768

Query: 802 IS--NTHNNNISPIITKIKYQDEDDGDFVVLGSDEDDWNVAKE 839  
 I + ++KY DEDGDF+ + SDED +A E  
 Sbjct: 769 IKLCGILKQAVPFRVRLKYVDEDDGDFITITSDDEDVLMFAE 808

CPU time: 0.26 user secs. 0.04 sys. secs 0.30 total secs.

Gapped

Lambda K H  
 0.270 0.0470 0.230

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 10384

Number of Sequences: 0

Number of extensions: 671

Number of successful extensions: 13

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 2

Length of query: 834

Length of database: 90,077,593

effective HSP length: 61

effective length of query: 773

effective length of database: 83489227

effective search space: 64537172471

effective search space used: 64537172471

T: 9

A: 40

X1: 16 ( 7.3 bits)

X2: 128 (49.9 bits)

X3: 128 (49.9 bits)

X1: 41 (21.7 bits)

X2: 73 (32.8 bits)

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Figure 8

5 Sc KLPVIASDDLKVCKKSIYDFIL (SEQ ID No 25)

++PV++SDDL++CKKS+YDF++

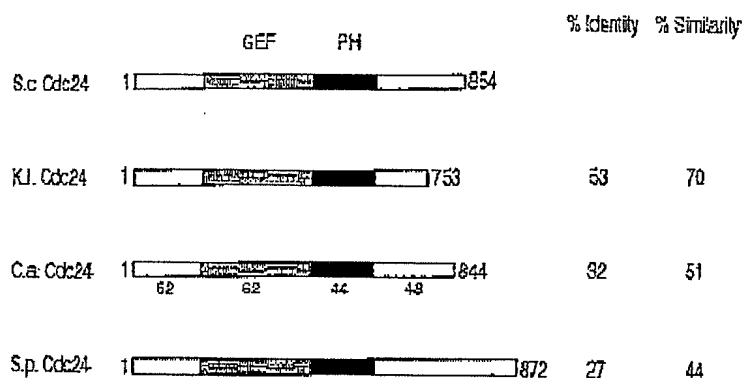
Ca QIPVVSSDDLRIKCKSVYDFLI (SEQ ID No 26)

10 Sc = *Saccharomyces cerevisiae*

Ca = *Candida albicans*

**A** **Fungal Cdc24's**

**figure 9**



## B

**Guanine nucleotide exchange factor domain of *CaCDC24* is homologous to other fungal Cdc24p's**

```

S.C. 227 S C A V E R T E R S T R I P P E D C O N T A I N I N G Q U I R K Q O S S I C K E R S V E L E R
X.# 237 N O D E I N C O N T A I N I N G V I D E O O F D I C T I O N ----- S C A L E O F C O N T A I N I N G
S.P. 277 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
-----
S.C. 387 V A L I D A T I O N S C H E M E S I N T E R N A T I O N A L C O N T A I N I N G Q U I R K Q O S S I C K E R S V E L E R
X.# 378 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
S.P. 377 V I D E O O F C O N T A I N I N G Q U I R K Q O S S I C K E R S V E L E R
-----
S.C. 347 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
X.# 347 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
C.# 344 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
D.P. 297 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
-----
S.C. 406 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
X.# 406 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
C.# 403 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
S.P. 353 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
-----
D.C. 455 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
X.# 455 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
C.# 463 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G
S.P. 403 S T A T E P A R A M E T E R S I N F I N A N C I A L S E C T O R ----- V I D E O O F C O N T A I N I N G

```

## C

### Homology of Stc4p binding region

```

S.c. 170 PCLILFNSHRECFILFVINSIDAK-----VICKSTVDELLGCKHVFANDEBELTISIDVFAN
K.l. 164 PLCLIFNVAFESQSLITVSSDPSG-----IINKSTVDELLGLCKHVFANDEBELTISIDVFAN
C.a. 180 PLCLILFNLITDSCITVWSSDDEK-----IANKSVDESLTAVITOLNEIDEMPTISIVFSP
S.p. 119 PLCLILNCHPVKESLWVNSSVLRKNTVQASLQFSEEMCLNEKQITIAALHSISLTQKP

S.c. 217 SLSQEVAVLEVMQVDMGSSSTLTPSKKTKQIMNAENQHRHQPSSSKKINLVAVETIEEL
K.l. 221 SLDHFLVDMVWNTLMAARVETQLDMGRLK-----S-GRAAPPTIDELGKEL
C.a. 237 NAQDTEEDLVINGLAEKSPDSTGGGDEDVH-----MDVQTITENSTVETRET
S.p. 179 SLPVPRVQOTLEMLKRYKNTHTSSSPSTDM--VPTGTHNSIASGRVATL

```

## D

### Homology of Bem1p binding region

```

S.p. 774 -----N T S S E I P H A I L Y E K V N F O D E I K A N S E I S N T H N N N I - S - P - I - K I - V O I
K.l. 789 -----D F Y N U S S I C H A R D I N A I K R G A H L S -----V I E K U V O I
C.a. 746 T P D - V A I F L Y K S I E L S E P T I O N A C T E Y N D L Q R I G O I T T S N I V A D N - N I S S E R V E
S.p. 768 S V R N T I N V I C R L R L B E V S L V E V Y A N D T E T E P A K V S H K I L C E I D K O N P P R V A L L N W I

```

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Figure 10

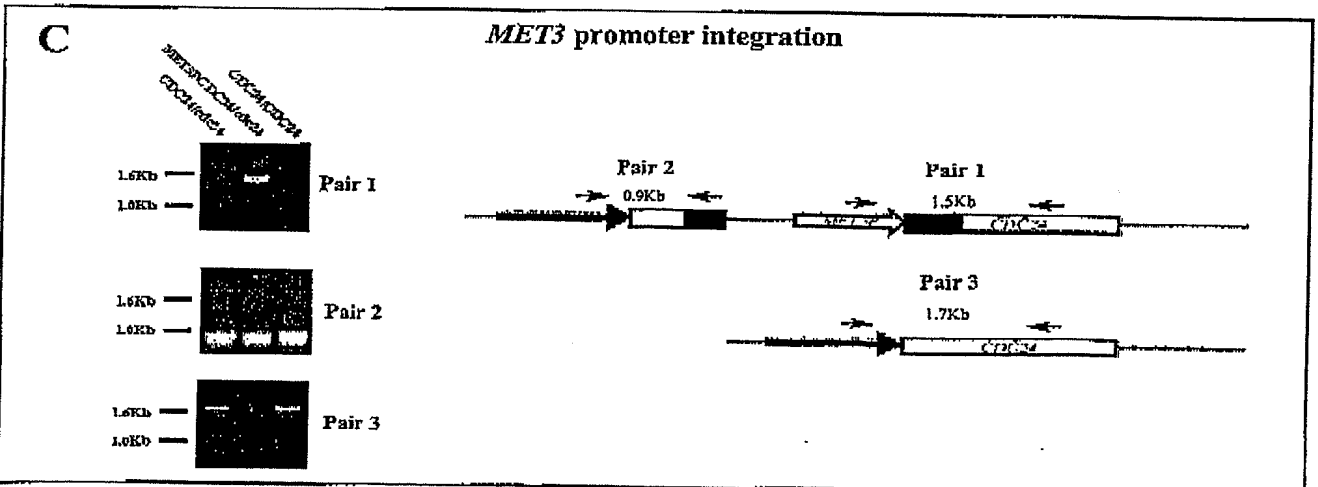
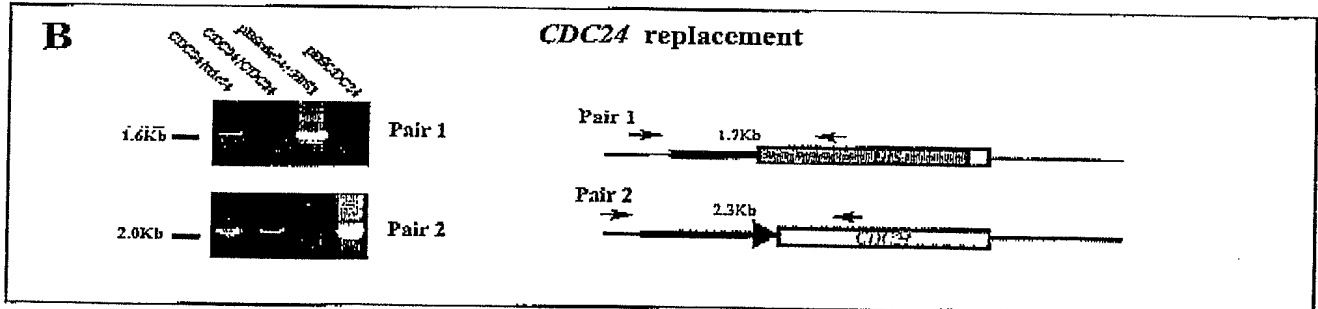
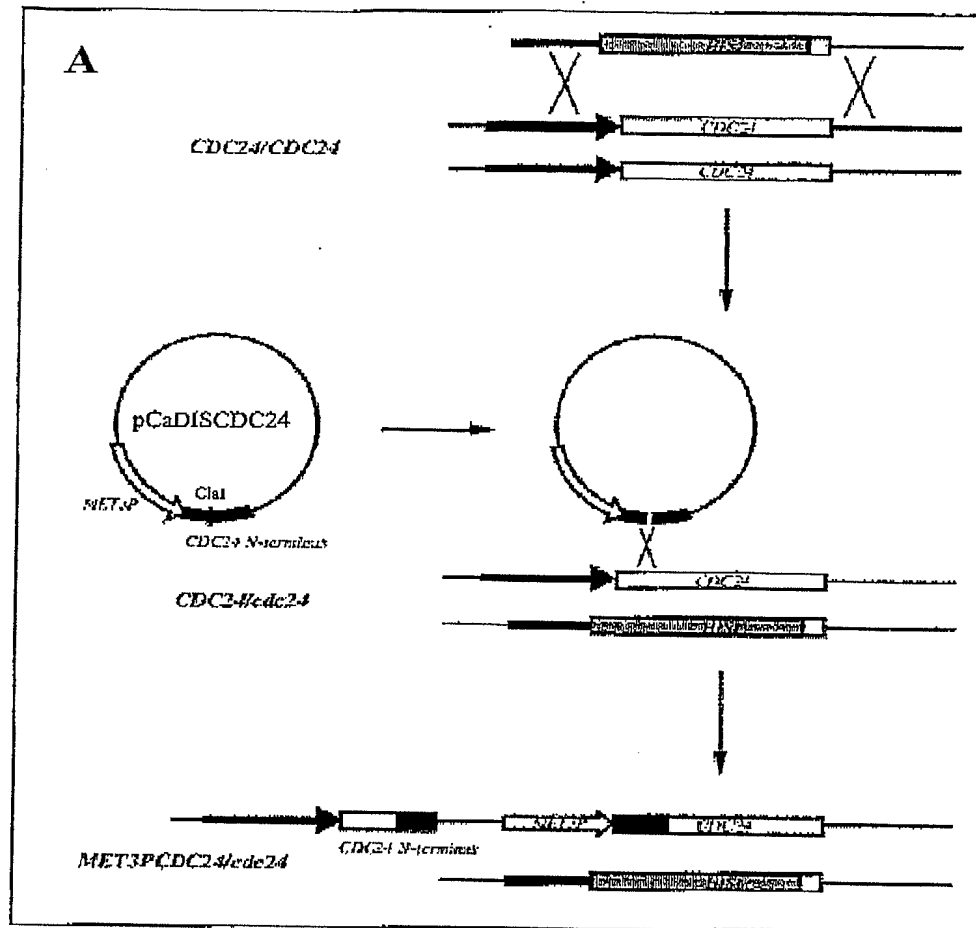
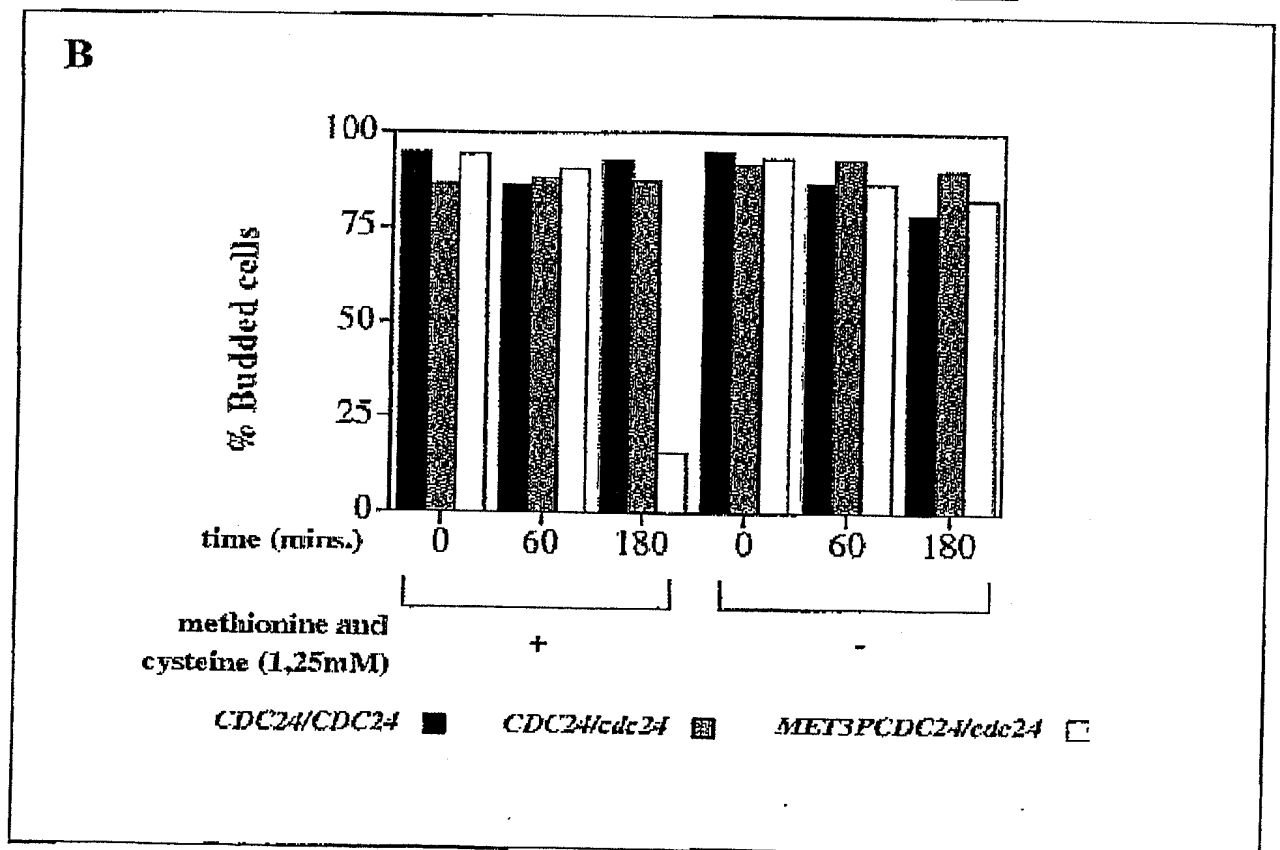
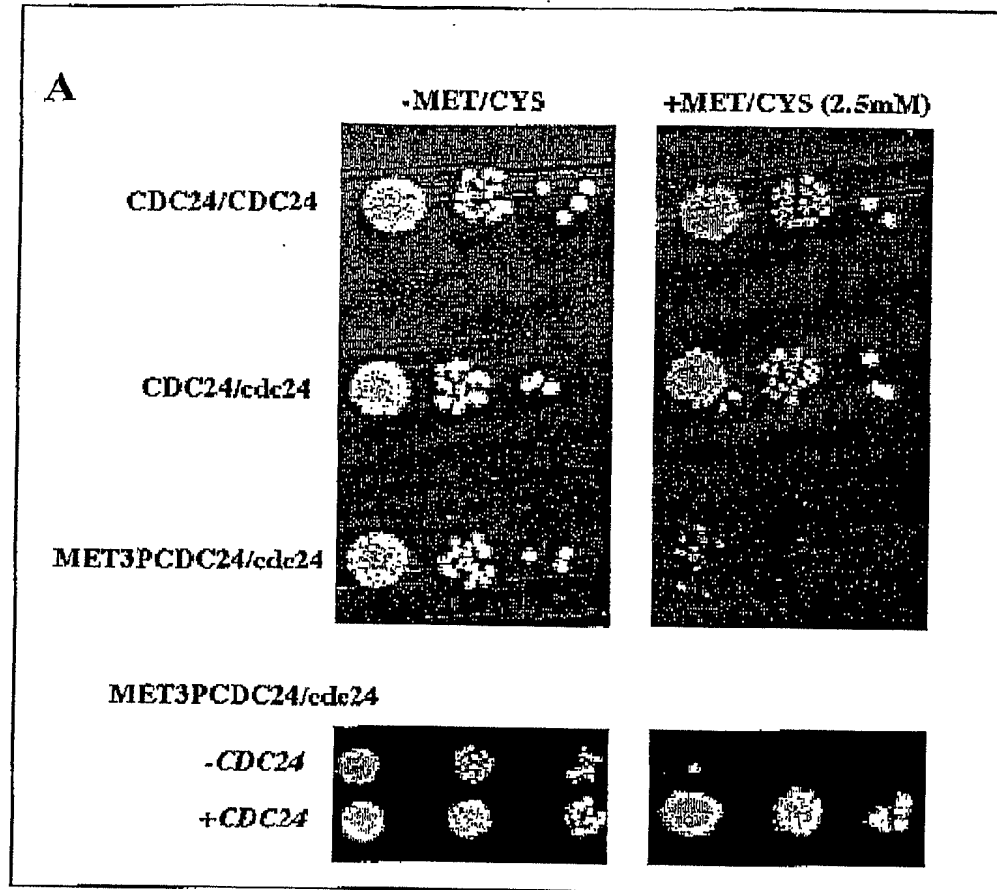


Figure 11



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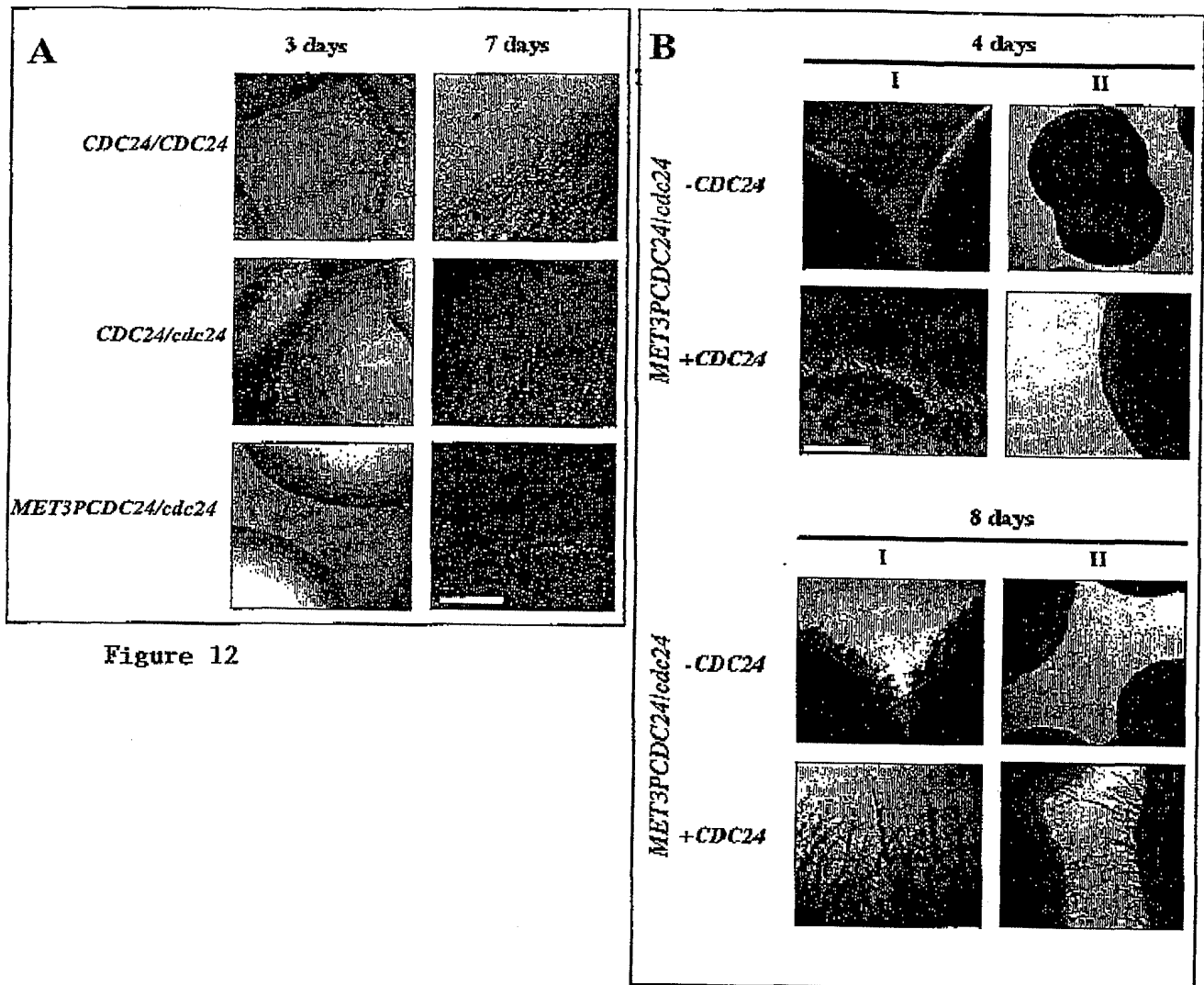
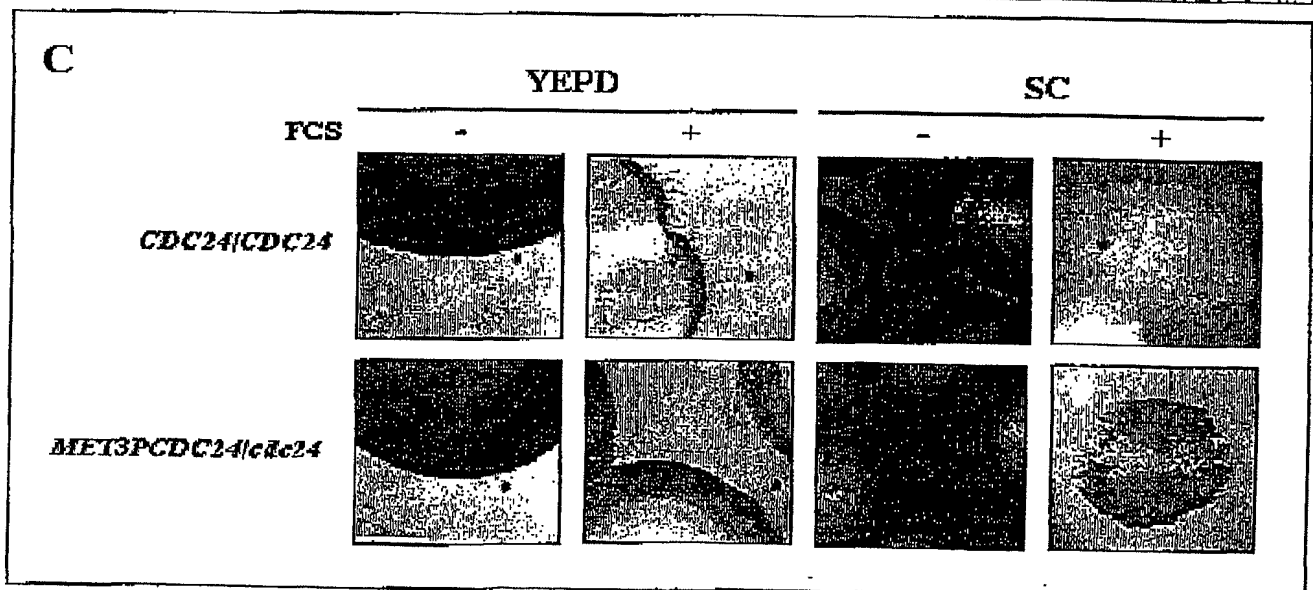


Figure 12





14A

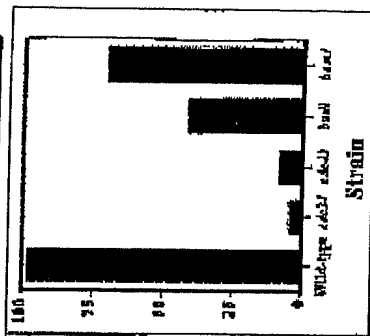
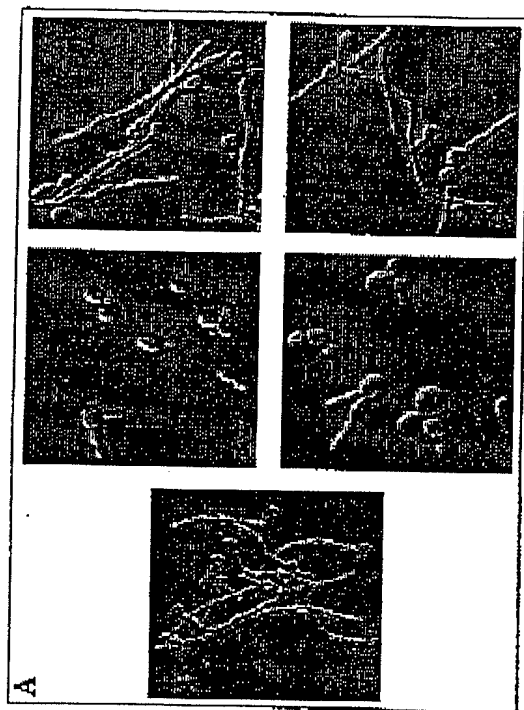


Figure 14B

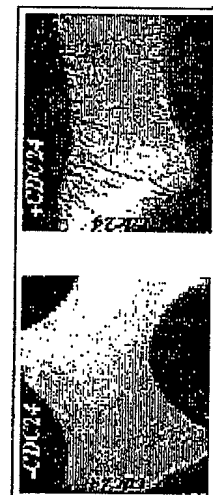
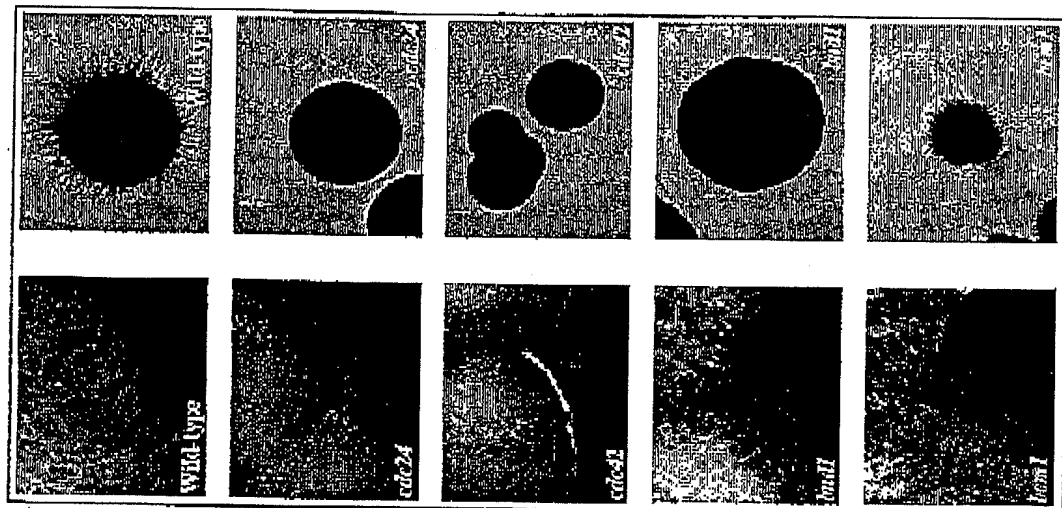


Figure 13

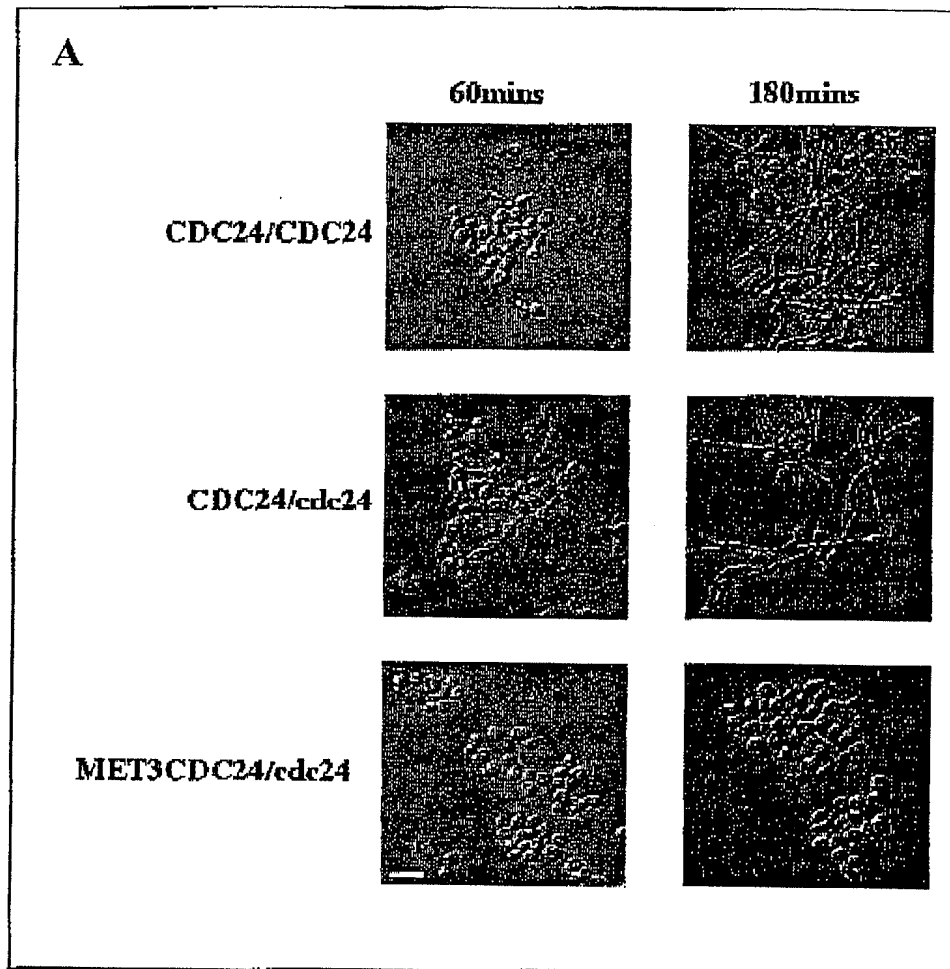
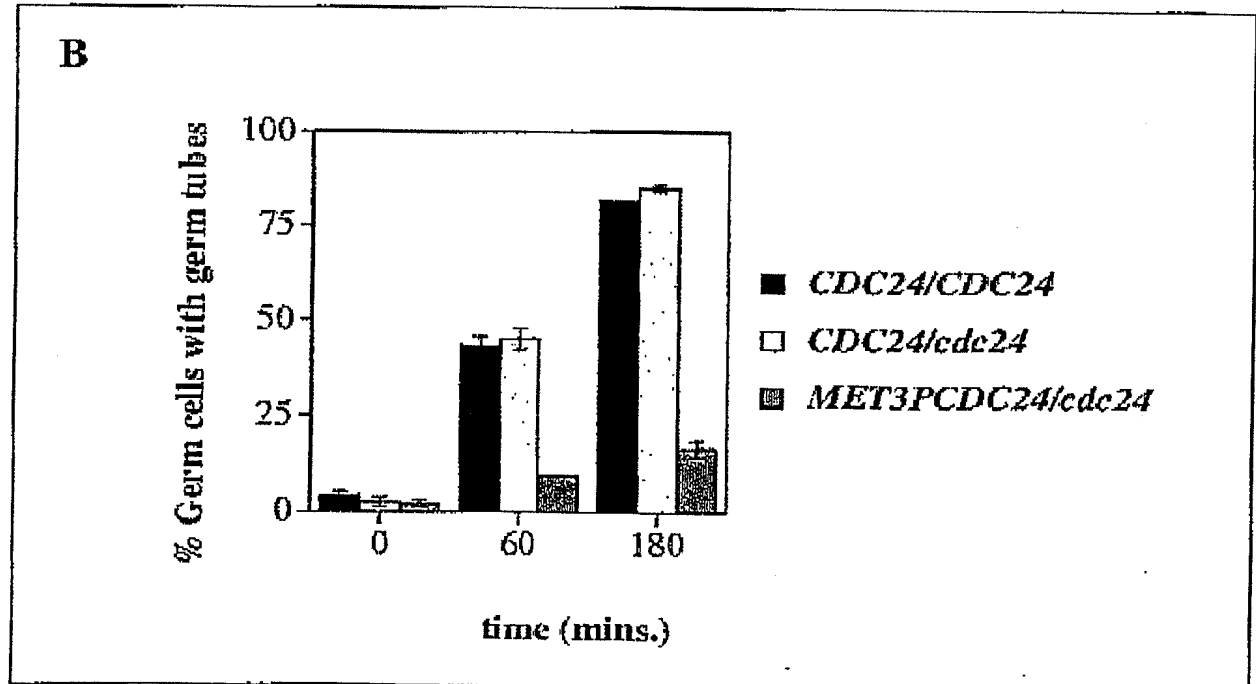
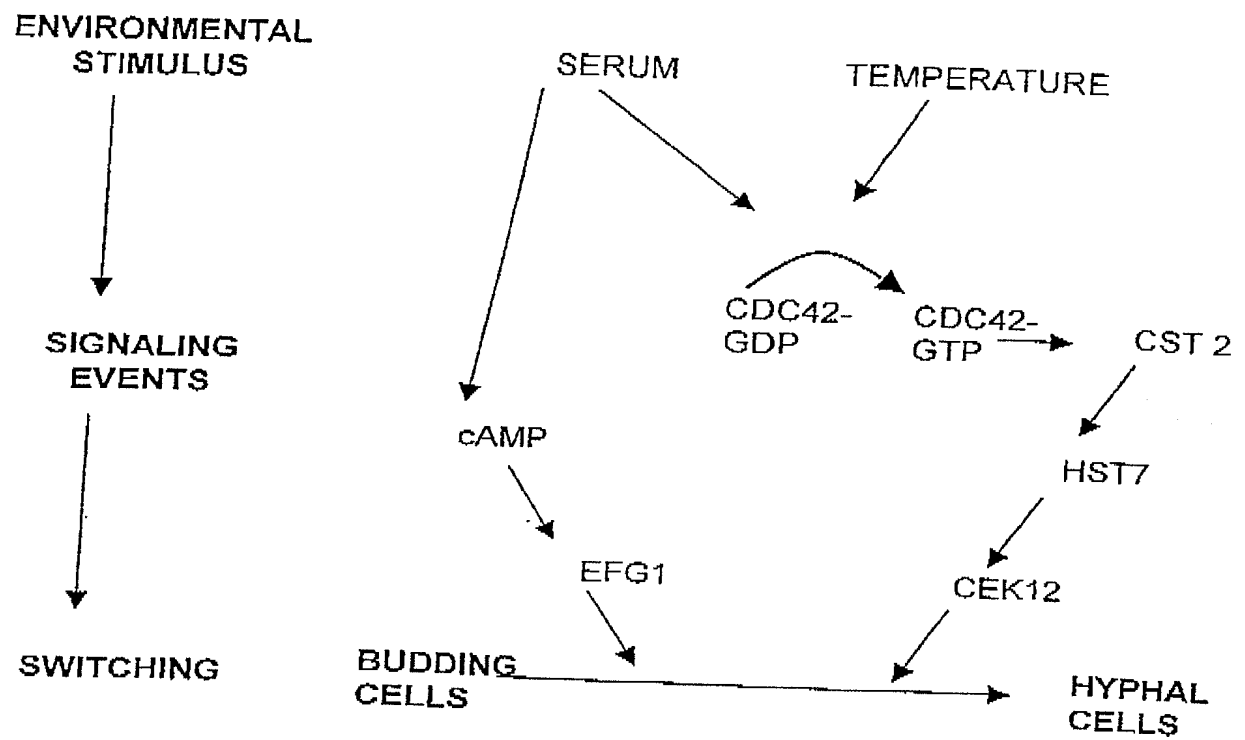


Figure 15



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Figure 16



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## Figure 17

A. *cdc24* (wt)

5

SEQ. I.D. NO:1

DNA:

ccccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcatctgacgattgaaagtctgtaaaaatccatttatgactt  
10 tatattgggctgcaagaaacactttgcatttaacgatgaggagcttttactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt  
gctagaagtagtagaaacgctaataatgaattccagc

SEQ. I.D. NO:2

Protein:

15 PLCILFNSVKPQFKLPVIASDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ  
LVKVLEVVEITLMNSS

B. *cdc24-m1*

20 SEQ. I.D. NO:3

DNA:

ccccctctgtatacttttcaactctgtgaagccgcaatttaaattaccggtaatagcattgacgattgaaagtctgtaaaaatccatttatgacttt  
atattgggctgcaagaaacactttgcatttaacgatgaggagcttttactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt  
gctagaagtagtagaaacgctaataatgaattccagc

25

SEQ. I.D. NO:4

Protein:

PLCILFNSVKPQFKLPVIAFDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ  
LVKVLEVVEITLMNSS

30

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C. *cdc24-m2*

5 SEQ. I.D. NO:5

DNA:

ccctctgtatactttcaactctgtgaagccgcaatttaaattaccggaatagcatctggcgatttgaaagtctgtaaaaatccattatgactt  
tatattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt  
gctagaagtagtagaaacgctaataatgaattccagc

10

SEQ. I.D. NO:6

Protein:

PLCILFNSVKPQFKLPVIASGDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ  
LVKVLEV VETLMNSS

15

D. *cdc24-m3*

SEQ. I.D. NO:7

DNA:

20 ccctctgtatactttcaactctgtgaagccgcaatttaaattaccggaatagcacctgacgatttgaaagtctgtaaaaatccattatgactt  
tatattgggctgcaagaaacactttgcatttaacgatgaggagctttcactatatccgacgttttgccaactcgacgtcccagctgggtcaaagt  
gctagaagtagtagaaacgctaataatgaattccagc

SEQ. I.D. NO:8

25 Protein:

PLCILFNSVKPQFKLPVIAPDDLKVCKKSIYDFILGCKKHFAFNDEELFTISDVFANSTSQ  
LVKVLEV VETLMNSS

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## SEQ ID NO. 10

## STE4 DNA sequence (wild-type)

ATGGCAGATCGATGGACTCGATAACGTATTCTAATAATGTCAACCAACAGTATATACAACCAACAGTCTACAGGA  
 TATCTCTGCACTGGAGGAGAAATTCAAATAAATAGAGGCCGCCAGACAGAGAGTAAACAGCTTCATGCTCAATATA  
 ATAAAGCAAAACACAAGATACAAGATGCAAGCTTATTCCAGATGGCCACAAAGTTACTTCGTTGACCAAAATAAGATC  
 5 AACTTAAGCCAAATATCGTGTGAAAGGCCATAATAAATATCTCAGATTTTCGGTGGAGTCCAGATTCAAACCGTAT  
 TTGAGTGCAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCCTTCAGGTTTAAACAGAGTCTATTCCATTAGATT  
 CTCATGGGGTTCTTTCCTGCGCTATTTCCGCCATCGAGTACTTTGGTAGCAAGCGCAGGATTAAACAATAACTGTACCATT  
 TATAGAGTTTCGAAGAAACAGAGTAGCGCAAPACGTTGCGTCAATTTTCAAAGGACATACTTGCTATATTTCTGACAT  
 TGAATTACAGATACGCGCATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAGCAAAGA  
 10 GGGTGAGAGATATTCTGACCATTAGGTGATGTTTTGSCATTAGCTATTCCTGAAGAGCCAACTTAGAAATTTCTTCG  
 AACACATTGCTAGCTGTGGATCAGACGGGTATACCTTACATATGGGATAGCAGATCTCCGTCCTCTGTACAAAGCTTTT  
 CTTAAGCAATGTATATTAATGCACTTCGTTTCTTCAAGACCTTCTGCTATTCTTCAAGTAACTGACATGCTTCG  
 TAAATATGTATCTTTAAGGTGGACTGTTCTATTGCTACTTTTCTCTTTTTCGAGGTTATGAAAGCTACCCCTACC  
 CCTACTTATATGGCAGCTATCATGGAGTACAATACCGCGCATCGCCACAACTTTAAATCAACAGCTCAAGCTATCT  
 15 AAGCAACCAAGGCGTTGTTCTTTAGATTTTAGTGCATCTGGAGATTGATGTAATCATGCTATACAGACATTGCTTGT  
 TTCTGTGGGATCTATTAAAGGAGAGATTGTTGCAAAATTAGAGGTCATGGTGGCAGAGTCACTGGTGTGCGCTCGAGT  
 CCAGATGGGTTAGCTGTATGTACAGGTTTCATGGGACTCAACCATGAAATATGGTCTCCAGGTTTCAATAG

20

## SEQ ID NO. 11

## Ste4 Protein sequence (wild-type)

MAEQMDSITYSNVNTQOYIQPQSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQMANK.TSLTKNKII  
 LKPNIVLKGEMNKISDFRWSRDSKRILSASQDGFMLIWDSASGLKQNAIFLDSQVWLSCAISPSESTLVASAGLNMNCTI  
 25 EVSKENRVAQNVASIFKGHTCYISDIEFTDNAHILTASGDMTCALWDIPKAKRVREYSDDLGCWALATFEENLENSI  
 TFASCGSDGYTYWDSRSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFQVEERTPT  
 TYMAANMEYNTRQSPQELKSTSSSYLDNQGVVSLDFASAGRLMYSCYTDIGCVVWDVLKGEIVEKLEGHGGRVTGVRES  
 DGLAVCTGSWDSTMKIWSPGYQ

30

## SEQ ID NO. 12

## ste4-o15 DNA sequence (mutant)

ATGGCAGATCGATGGACTCGATAACGTATTCTAATAATGTCAACCAACAGTATATACAACCAACAGTCTACAGGA  
 35 TATCTCTGCACTGGAGGAGAAATTCAAATAAATAGAGGCCGCCAGACAGAGAGTAAACAGCTTCATGCTCAATATA  
 ATAAAGCAAAACACAAGATACAAGATGCAAGCTTATTCCAGATGGCCACAAAGTTACTTCGTTGACCAAAATAAGATC  
 AACTTAAGCCAAATATCGTGTGAAAGGCCATAATAAATAAATCTCAGATTTTCGGTGGAGTCCAGATTCAAACCGT

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TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCCTTCAGGTTTAAAACAGAACGCTATTCCATTAGAT  
 CTCATGGGTTCTTTCCTGCGCTATTTCCGCATCGAGTACTTTGGTAGCAAGCGCAGGATTAAACATAACTGTACCAI  
 TATAGAGTTTCGAAAGAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAAGGACATACTTGCTATATTTCTGACA  
 TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAG  
 5 GGGTGAGAGGATATTCTGACCATTTAGGTGATGTTTTGGCATTAGCTATTCTGAAGAGCCAACTTAGAAAATTCTTC  
 AACACATTCCGTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCCGCTGTACAAAGCTTTT  
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 TAAATATGTATGATTTAAGGTCGGACTGTTCTATTGCTACTTTTTCTCTTTTTCGAGGTTATGAAGAAGCTACCCCTAC  
 CCTACTTATATGGCAGCTAACATGGAGTACAATACCGCGCAATCGCCACAACTTTAAATCAACAAGCTCAAGCTATC  
 10 AGACAACCAAGGCGTTGTTTTCTTTAGATTTTAGTGCACTCTGGAAGATTGATGTAATCATGCTATACAGACATTGGTTGT  
 TTGTGTGGGATGTATTAAAGCAGAGATTGTTGGAAAATTAGAAGGTCATGCTGGCAGAGTCACTGGTGTGCGCTCGAG  
 CCAGATGGGTTAGCTGTATGTACAGGTTGATGGGACTCAACTATGAATATATGGTCTCCAGGTTATTAATG

SEQ ID No. 13

15 Ste4-o15 Protein sequence (mutant)

MAHQMSITYSNNVTQYYIQPSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQANKVTSLSLTKNK  
 LKPNIVLKGNHNNKISDFRWSRDSKRILSASQDGFMLIWDASGLKQNAIPLDSQWVLSCAISPESTLVASAGLNNNCT  
 RVSKENRVAQNVAIFKGHTCYISDIEFTDNAHILASGDMTCALWDIPKAKRVRGYSOHLGDVLAALAFEEPNLENS  
 20 TFASCGSDGYTYIWDSSPSAVQSFYVNDSDINALRFFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTP  
 TYMAANMEYNTAQSPQTLKSTSSSYLDNQGVVSLDFSASGRMLMYSCYTDIGCVVWDVLKGEIVGKLEGHGGRVTGVRV  
 DGLAVCTGSWDSTMKIWSPGYQ

SEQ ID NO. 14

25 ste4-o17 DNA sequence (mutant)

ATGGCACATCAGATGGACTCGATAACGTATTCTAATAATGTACCCCAACAGTATATACACCCACAAAGTCTACAGGA  
 TATCTCTGCAGTGGAGGAAGAAATTCAAAATAAAATAGAGGCCGCCAGACAAGAGAGTAACAGCTTCATGCTCAAAT  
 ATAAAGCAAAACACAAGATACAAGATGCAAGCTTATCCAGATGGCCAAACAAAGTTACTTCGTTGACCAAAATAGAT  
 30 AACTTAAAGCCAAATATCGTGTGAAAGGCCATAATAATAAAATCTCAGATTTTCGGTGGAGTCGAGATTCAAAACGTA  
 TTTGAGTGCAAGTCAAGATGGCTTTATGCTTATATGGGACAGTGCCTTCAGGTTTAAAACAGAACGCTATTCCATTAGAT  
 CTCATGGGTTCTTTCCTGCGCTATTTCCGCATCGAGTACTTTGGTAGCAAGCGCAGGATTAAACATAACTGTACCAT  
 TATAGAGTTTCGAAAGAAACAGAGTAGCGCAAAACGTTGCGTCAATTTTCAAAGGACATACTTGCTATATTTCTGACA  
 TGAATTTACAGATAACGCACATATATTGACAGCAAGTGGGGATATGACATGTGCCTTGTGGGATATACCGAAAGCAAAG  
 35 GGGTGAGAGGAATATTCTGACCATTTAGGTGATGTTTTGGCATTAGCTATTCTGAAGAGCCAAACTTAGAAAATTCTTC  
 AACACATTCCGTAGCTGTGGATCAGACGGGTATACTTACATATGGGATAGCAGATCTCCGTCCGCTGTACAAAGCTTT  
 CGTTAACGATAGTGATATTAATGCACTTCGTTTTTTCAAAGACGGGATGTCGATTGTTGCAGGAAGTGACAATGGTGCG

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TAAATATGTATGATTTAAGGTCGGACTGTTCTATTGCTACTTTTTCTCTTTTTCGAGGTTATGAAGAACGTACCCCTACC  
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 AGACAACCAAGGCGCTGTTTCTTTAGATTTTAGTGTCATCTGGAAGATTGATGTACTCATGCTATACAGACATTGGTTGTC  
 TTGTGTGGGATGTATTAAAAGGAGAGATTGTTGGAAAATTAGAAGGTCATGGTGGCAGAGTCACTSGTGTGCGCTCGAGT  
 5 CCAGATGGGTTAGCTGTATGTACAGGTTTCATGGGACTCAACCATGAAAATATGGTCTCCAGGTTATCAATAG

SEQ ID No. 15

Ste4-o17 Protein sequence (mutant)

10 MAHQMDSITYSNNVTQQYIQPSLQDISAVEEEIQNKIEAARQESKQLHAQINKAKHKIQDASLFQMANKVTSLTKNKI  
 LKFNIVLKGHNKISDFRWSRDSKRILSASQDGFMLIWDSASGLKQNAIFLDSQWVLSCAISPSSTLVASAGLNNNCTI  
 RVSKENRVAQNVAIFKQHTCYISDIEFTDNAHILTAGDMTCALWDIPKAKRVREYSDELGDVLAIAIPEEPNLENSI  
 TFASCGSDGYTYIWDSRSPSAVQSFYVNDSDINALREFKDGMSIVAGSDNGAINMYDLRSDCSIATFSLFRGYEERTPT  
 TYMAANMEYNATAQSPQTLKSTSSSYLDNQGAVSLDFSASGRIMYSCYTDIGCVVWDVLKGEIVGKEEGHGGRTGVRS  
 15 DGLAVCTGSWDSTMKIWSPGYQ

SEQ. I.D. No:16 refers to the epitope sequence "Tyr Pro Tyr Asp Val Pro Asp Tyr Ala".

SEQ. I.D. No:17 refers to TEV protease recognition sequence "Gln Asn Leu Tyr Phe Gln Gly"

SEQ. I.D. No:18 refers to peptide sequence "QFKLPVIAFDDLKVCKKSI".

SEQ. I.D. No:19 refers to peptide sequence "QFKLPVIASGDLKVCKKSI".

SEQ. I.D. No:20 refers to peptide sequence "QFKLPVIAPDDLKVCKKSI".

SEQ. I.D. No:21 refers to peptide sequence "QFKLPVIASDDLKVCKKSI".

SEQ. I.D. No:22 refers to peptide sequence "QYEFDVILSPELVQMKTII".